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NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC heip deek Email: Cgapbe-Kmmail.nih.gov	001) Nation 1), Cancer Drive, Ro	obos espiens. Nomo espiens Sukaryota: Metasoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota: Metasia; Prinates; Catarrini; Mondiidas; Homo.	BCC107386   931 bp mRNA linear PRI 29-CCT-2001   PROMO applene, ribosomal potesti St, Y-linked, Clone MCC:5070   PRI 20108329, mRNA, complete Cds.   PRI 20108329   PRI 2010788   PRI 20	ANGCORANGECOTOCHGANAFTENCHAGASTTOCT 685	3.24; Score 39; DB 2; Length 154330; Similarity 100.04; Pred, No. 1.7ev-10; 19; Conservative 0; Mismarches 0; Indels 0; Gaps 0;	/chizemascme="3". /clone="62NBb006F09" 43409 m 33401 C 33798 G 43714 t 10 others	139679 154330. contrig of 14652 bp in length. Location/Qualifices 1154330 15450 15	of 1058 of 1058 unknown of 4188	94650: contig of 7329 bp gap of unknown len gap of unknown len gap of unknown len 96734: contig of 2084 bp	s woon as it is be preserved. of 1981 bp in 1 unknown length of 30691 bp in unknown length	submitted (11-202-2021) Clempon University demonits Institute.  (Common This sail, Yand Dad Sail to seventee at Leventy John - consists of 8 contigs days between the contigs - an apprehensic a mana of N. The contigs of the places - an apprehensic a mana of N. The contigs of the places - of the place been time are based on estances that have - provided by the measurer.	Same A.C., Henry, D., Ostes, R. and Simons, J.  Number of Sevence  Outpublished Sevence  Outpublished Sevence  Outpublished Sevence  Number of Sevence Sevence  Number of Sevence Seve
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Connact: villalonBom.Exc. Naile. S.M., Hulyk. S., Lu, X., Garcia,
VALLA Hollowey, M., Telford, B., Hodgeon, A., Bouck, J., Yu, W.,
Muzzy, D.M., Gibbs, A.M.
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REFERENCE JOURNAL MEDLINE PUBMED REFERENCE

AUTHORS

2 (bases 1 to 116696) Mungall, K., Bowman, S., Churcher Rajandream, M.-A. and Barrell, B.

Churcher, C., Lawson, D.,

10448855

Nature 400 (6744), 532-538 (1999)

The complete nucleotide sequence of chromosome 3 of Plasmodium

talciparum

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Lawson,D., Bowman,S. and Barrell,B Direct Submission

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// moree:"PE00445W, WALIPA:24', conserved hypothetical
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Bayuslaviy, L., Bookagater, B., Beron A., Backer, G., Gorte, A.,
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Berestiani, C., Bayusla, M., Porrest, C., Gage, D., Galagan, J.,
Bardona, S., Gorte, G., Bayusla, M., Borton, D., Karten, M.,
Bardona, J., C., Loudman, M., Loude, J., Loren, L., Karten, M.,
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Brojinovici, N., Subtamanian, K., Talaman, J., Terdayo, S., Thodore, J.,
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Brother, A., and Boy, M., Well, R., Vol, A., Wu, X., Wyman, D., Ye, M.,
Brother, A., and Boy, M.,
substitted (0f-FBS-2000) Mitteland Institute/MIT Center for Genome Research, 200 Charles Stroner, Cambridge, MA 2114, USA. On Oll 13, 2000 this segmence various replaced gi-8918916. All repeate were identified unling RepeateMent State, A.P. A. 6 Green, P. (1995-1997) State, A.P. A. 6 Green,
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212: gap of 100 bp 21885: contig of 673 bp in length 985: gap of 100 bp

11664 11763; gap of 100 bp
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Patent: WO 0107661-A 7 01-FEB-2001;
Gen-Probe Incorporated (US)
        /note="assembly_fragment"
78132. .86641
/note="assembly_fragment"
86142. .97779
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97880. .106798
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Bularyota Netrasa, Aftiropoda, Hoaspoda; Insecta; Françoca;
Bularyota Netrasa, Aftiropoda, Hoaspoda; Insecta; Perceptia
Bodracidas; Dossophilidas; Desaphilia
Bodracidas; Desaphilidas; Desaphil
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AV11949
EX113949.1 GI:21428767
This clone was sequenced as part of a high-throughput process to sequence 2000 mis may prove the control of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lawrence Berkeley Metional Laboratory One Cyclotron Hobble Berkeley, CO, 94720, USA
Sequence aubmitted by:
Berkeley Drosphila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA, 94720, Metional Laboratory
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These we halkers the sequence to satisfact enhanced with the following the control of the satisfact enhanced with pitch officers that collection between the satisfact with pitch officers and satisfact and jumes with a literal pointing, printing from commandating genomic tows, resulted and room reverse transcriptance errors that results in single have changes are printed in the collection of the
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prining, priming from conteminating genomic DWA, restained introme due to reverse transcription of unspileed preverse TWA-a and reverse transcriptance errors that result in single hase changes. For further information about this sequence, including its location and relationship to other sequences, please visit our Web site thrip///frinitry/punks/by_coll) or send meable to
cdna@fruitfly.berkeley.edu.
Location/Qualifiers
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misc\_feature /note="Longest ORF" /organism="Drosophila melanogaster" /db\_xref="taxon:7227" /note="sim4 alignment with AE003598 (band-79E4-band-79F3)"

source

/translation="MPPKPKHRDVAGFLSRVRNFLLGRTHKTAHRFADMVSPRTQPPP /protein\_id="AAM50103.1" /db\_xref="GI:21428768" /product="AT13913p"

Matches Guery Match Best Local Local Similarity 302 2.8%; Score 34; DB ilarity 100.0%; Pred. No. 1e Conservative 0; Mismatches 20 NIPSGPTQSLFANYYYTRDPRRLVKPFVDVVQEHKKMLTAKVKEEEAAKKAQAKSGDA PKDGSPIPPVGPKTTDTNECDEGNSGAKKLPTPGKVHSWEGPH" 208 c 164 t DB 3; le-07; Length 853 c Gaps

1184 CGTTTAMAMAAAAAAAAAAAAAAAAAA 1217

754 CGTTTMAMAAAAAAAAAAAAAAAAAAAA 787

KEYWOKUS VERSION ACCESSION DEFINITION LOCUS AY060916 Drosophila melanogaster GM06077 full length cDNA AY060916 AY060916.1 GI:16768489 AY060916 å BKNA INV 08-NQV-2001

ORGANISM

AUTHORS HILCHAN, malandament 
Discounting management and management in macras, Penyaputa, 
Bakaryota, Menanda, Anthropoda, Hoxapoda, Inapeta, 
Meophera, Hendreds, Marthropoda, Hoxapoda, 
Meophera, Indepenyaputa, Dipetas, Brachhyones, Mascountphi, 
Dhamada, Draspathildae; Dosephila, 
Dhamada, Draspathildae; Dosephila, 
Sapleton, M. Bodsesti, P. Kopi, L. Addayyahi, A. Carleon, J., 
Sapleton, M. Bodsesti, P. Kopi, L. Addayyahi, A. Carleon, J., 
Ganga, M. Chavas, C. Dosephila, D. Fries, B. George, R. 
Management, Bachda, J. Harbara, M. Luco, M. Menada, A. Mangali, C. J. 
Management, Bachda, J. Harbara, M. Luco, M. Menada, M. Mangali, C. J. 
M. V. L. Levis, S. E. Rabin, A. M. and Callider, S. 
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JOURNAL TITLE

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This close was selected for full length sequenting because it practings to the following selection criteria: matched dBM gi: 4557454.  PRACTINES  FRACTIONS  FRACTIONS  FRACTION  FRACTION	COORD_GENERAL   CONDITION KINNER   FOODST-SENIAL   CONDITION KINNER   FOODST-SENIAL	Opery Macch as a construct of the construction	RESERVE 15 AUTOFILE LOCATION AND THE MEMBERS AND THREAT TWO 20-DEC-2001 LOCATION DESCRIPTION DESCRIPTION AND THREAT TWO 20-DEC-2001 LOCATION DESCRIPTION DESCRIPTI	REFERENCE 1 (Benes 1 to 1771).  AUTHORS Scalicon M. Brocketchip P., Medry L., Adaywal, A., Carlson, J., Park, S., Patel, S., Carlson, J., Carlson, J., Carlson, J., Carlson, J., Patel, S., Carlson, J., Carlson, J.	
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Best Local Similarity 100.0%; Pred. No. 1e-07;
Marches 34; Conservative 0; Mismatches 0; Indels
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/note="alignment with genomic scaffold AE003589"
/db wref="FLYBASE:FBgn0031260"
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phosphosulfate kinase, useful for altering expression of sulfate
assimilation protein in plants
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840

601

TGATGGTGACAACCTCAGACATGGCCTAAATAGAGATTTAAGCTTTAAGGCAGAAGACCG

Rosen CA,

Ruben SM

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(i.e. selecting a composition for inthiteing procease cancer in a patient; (i) assessing the protecte call cardinopalic potential of a compound; (i) determining whether prostate cancer has mestastaited in a patient; (ii) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                      Novel isolated nucleic acid molecule associated with cancerous state of prosetae cells and correlating with presence of prosetae ancer, useful foor detecting presence of prostate cancer, stage of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting and quantitating analyte polymucleotide in a sample, by co-amplifying analyte polymucleotide with predetermined amount of speudo target, producing amplification products and quantifying analyte
                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated muclie cald molecule [1] computed an autocontic sequence given in Tables 1-9 (MR000ID-A807221) of the specification or its complement. [1] as setul (or is setul or its according to the complement of a setul or its period of the complement of a setul or its period or is setul or its period or its peri
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    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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35; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probe #3 used in a method for
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                                                                                                                                                            Schlegel R. Endege WO.
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                                                                                                                                                                                                                   WPT: 2001-662795/76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe; HIV; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200107661-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF60546:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amplicons
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us-09-720-384a-3.oli.rnq
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                                                                                                                                                                                                                                                                                                                                                                                           process; called paccracic concer writegos; given in Addison concernor concernor account of the Management of the Managem
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pharmacogenomic marker, gene, 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                               New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or for use in assay 8 for diagnosing a pathological condition cancer, or for use in assay 8 for diagnosing a pathological condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.0%; Score 36, DB 21, Longth 2952;
.00.0%; Prod. No. 9e-05,
.ve 0, Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2952 BP, 766 A, 645 C, 671 G, 868 T, 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2916 TTCGTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 696-697; 1379pp; English
Wed Dec 18 10:26:16 2002
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2000US-219007P.
2000US-255281P.
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16-MAR-2000, 2000US-189862P.
25-MAY-2000, 2000US-207454P.
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Matches 36; Conservative
                                                                                                                                                      WPI; 2000-579444/54.
P-PSDB; AAB54264.
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Matches
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                                                                                                                                                                                                                                           The present invention provides probes and PCR primers for use in the detection of HTV. These are shown in AMPSSS39. AMPSSS99. They can be used to disgnose HTV infection and to ensure that blood and blood used to disgnose HTV infection and to ensure that blood and blood products do not company the yivaw, thus enabling the presention of HTV
                                                                                                                                                                                                                                                                                                                                                                                                     Detecting HIV-1 nucleic acids in biological samples useful for
diagnosing HIV-1 infection involves using nucleic acid capture
oligomers, amplification oligomers and probe oligomers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bee
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                                             1184 CGTTTMUMAMMAAAAAAAAAAAAAAAAAAAA 1217
                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 50; 60pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIV-1 detection
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                                                                                                                                                                                Sequence 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MCDO/ J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WC200104361-A2
                                                                                                                                                                                                                         infection during blood transfusions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BEEG/)
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CGTTTAAAAAAAAAAAAAAAAAAAA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection; diagnosis;
                                                                                 ch 2.8%; Score 34;
l Similarity 100.0%; Pred. No.
34; Conservative 0; Mismatc
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34; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MCDONOUGH S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEN-PROBE INC
BEE G G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yang YY, Kolk
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Unity 100.0%;
Conservative o
                                                                                                                                                                                BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      blood screening;
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Pred. No. 0.0011;
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                                                                                          Mismatches
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                                                                                     DB 22;
. 0.0011;
ches 0;
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                                                                                     Gaps
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Matches 34
                                                                                                                                                                                                                                                                                                                                                                                                     main invention relates to a series of muchica acid chipomers for applifying and descripting a muchacida sequence of human improved chipment of the control o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gag and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV; human immunodeficiency virus; ss; probe; gag; protease; reverse transcriptase; infection.
                                                                                                                                                                                                           1184 CGTTTAGAAAAAAAAAAAAAAAAAAAAAAA 1217
                                                                                                                                                                                                                                                                                                                                              Sequence 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid oligomers for amplifying a nucleotide sequence from
HIV-1 and probes for detecting the amplified product are specific for
gag and pol regions and are useful to detect different subtypes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-SEP-2000; 2000US-229790P
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                                             AAL45493 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BREN/) BRENTANO S T.
(BABO/) BABOLA O.
(TRAN/) TRAN N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (YANG/) YANG Y Y
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                                                                                                                                                                                                                                                                                                                                                                                       invention
                                                                                                                                                              CGTTTABAAAAAAAAAAAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                          BP; 35 A; 8 C; 4 G; 10 T; 0 other;
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                                             DNA;
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                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                          Score 34; DB 24;
; Pred. No. 0.0011
                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vernet
                                                                                                                                                                                                                                                                                             Length 57;
                                                                                                                                                                                                                                                    Indels
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Gaps

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us-09-720-384a-3.oli.rng

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The strengton relates to an insoluted markets eated molecule (1) comprising a mutilectide segmence given in Tables 1-9 (AWVORD)-AWK2213) of the specification of its complement. (1) is useful fortune specification of the complement. (1) is useful fortune search for the complement in the progression of professed with prostate consert (1) enteresting the progression of professed cancer in a patient fitting of a sear compound to inhibit prostate cancer in a patient; failing of a sear compound to inhibit prostate cancer in a patient; failing of a star compound to inhibit prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; oryotine; call profiteration; call differentiation; gene therapy; varieties prepriete therapy; steen call growth factor; hasmatopisess; attaining provide factor; hamilmondulatory; cancer; leuksemia; attaining provide factor; hamilmondulatory; cancer; leuksemia; attaining provide green disorders; attaining steen; leuksemia; attaining steen disorders; attaining steen; atta
                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acid molecule associated with cancerous state of prostate cates. In setal prostate cateer, is setal for detecting presence of prostate cancer. Is setal for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is electring a composition for inhibiting proceate cancer in a patient; (a assessing the proceate cancer in a patient; (g) determining whether proteate cancer has esseatisfal of a compound; (g) determining whether proteate cancer has esseatisfal and appressiveness or incidence of proceate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.8%; Score 34; DB 23; Length 310; Best Local Similarity 100.0%; Pred. No. 0.00002. Meethes 34; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 310 BP; 101 A; 57 C; 38 G; 114 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 11710; 11750pp; English.
                                                                                                                                                                                                          Schlegel R, Endege WO, Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human polynucleotide SEQ ID NO 7463.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAI87403 standard: cDNA: 407 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT, Liu C, Drmanac RT;
09-JUN-2000, 2000US-211314P.
18-JUL-2000, 2000US-219007P.
13-DEC-2000, 2000US-25581P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-FEB-2001, 2001WO-US04927.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-MAY-2000; 2000US-0577409
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                                                                                                                                                                                                                                                                       WPI; 2001-662795/76.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200164835-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA187403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 patient
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                                                                                                                                             HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a number of numbers end oligeness which
can be used to smplity that age and poligenes of human immunosediteitency
vivitor kypt [1874]. They are are used to deter regions of the age and pol
genes, especially regions associated with dumy resistance, and also for
cleantifying agentic subviyes of the virus. The present sequence is an
oligener, the invention.
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pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid oligomer, useful for detecting selected regions of gag
and pol genes of human immune deficiency virus, particularly for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gans
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Local Similarity 10.0%; Pred. No. 0.0011.
se . 34; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tran N, Vernet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and pol genes of human immune deficiency virus, assessing drug resistance
                                                                                                     HIV-1 RNA capture oligonucleotide SEO ID NO: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 57 BP; 35 A; 8 C; 4 G; 10 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTTTABABABABABABABABABABABABABA 1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human prostate expression marker cDNA 61930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 CGTTTBABABABABABABABABABABABABA 56
                                                                                                                                                                                                                                                                       Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Babola O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; Page 57; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABV61939 standard; cDNA; 310 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-SEP-2000: 2000MO-US24117.
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16-MAR-2000, 2000US-189862P.
25-MAY-2000, 2000US-207454P.
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                                        06-JUN-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yang YY, Brentano ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BIOMERIEUX SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENP-) GEN-PROBE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                       14-MAR-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INME
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Claim 1, Page 51-52, 65pp; English

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Query Match
Best Local S
Matches 34
                                                                         Comprising
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                                                                                                                                                                                           P-950B, AAB48724, AAB48725, AAB48726, AAB48727, AAB48728, AAB48729,
AAB48730, AAB48731, AAB48732, AAB48733, AAB48734, AAB48735, AAB48736
AAB48737, AAB48738, AAB48739.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nouse; growth hormone; GH regulatable gume; liver pathology; hypertcophy; hepatocollular leason; hyperplasia, eltered expression level; lone 5; hepatocollular leason; hyperplasia, eltered expression level; lone 5; dagmonic marker; gigantism; sercesgaly; diabetes; hapatocropic; transpanic animal; drug acreening; drug discovery; marino; se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC87257 standard; cDNA; 1908 BF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acids and polypeptides, diagnosing and treating e.g. leukaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYOH-) UNIV OHIO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse liver growth hormone-induced cDNA clone 5, SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 407 BP; 165 A; 65 C; 80 G; 83 T; 14 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nes 34; Conserv
                                                                                                                                                                                                                                                                                                                              2001-007239/01
abnormal levels of growth hormone activity in liver assaying growth transcriptional activity and protein level of hormone-regulatable liver genes, as diagnostic liver pathology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       Lip Guot.
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; Length 407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inflammation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.00078;
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consist horses (set) activity in the livet. For predicting a chase it the condition of the livet in expression of certain specific genes and other properties of the certain specific genes (the condition of the livet of the pression of certain specific genes (the condition of the livet as the centic of an activity processing of the livet is the condition of the livet as the centic of an activity processing of the certain specific genes (the condition of the livet as the centic of an activity processing the centic of the centic of
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Matches
             Best Local Similarity
                                                    Sequence 1908 BP; 525 A; 475 C; 477 G; 431 T; 0 other;
2.8%; Score 34;
ilarity 100.0%; Pred. No.
Conservative 0; Mismatc
  Mismatches
. 0.00058,
                        DB 22; Length 1908;
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MASZII
                                                                                     1814 ССТТИЛИМИЛИМАЛИМАЛИМАЛИМАЛАМАЛА 1847
                                                                                                                    AAA52773 standard; cDNA; 2040
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Soybean; carbon catabolite repression; sucrose non-fermenting protein l; SNF1; plant growth; se.
                                                                                                                            Soybean putative catabolite repression protein SNF1 coding sequence #3.
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03-JAN-2001

(first entry)

Glycine max Location/Qualifiers 360..1676 /\*tag= a

W0200036115-A2

/product= "SNF1"

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The present invention provides a number of mann immed system seccieted genera which are sodified by the settly size of consistes. The sospence afficiency of cyclesines. The sospence afficiency of cyclesines, The sospence afficiency of diseases show a settlines of size sections are settlines for the cyclesines and a settlines of cyclesines are settlines of the cyclesines and a settlines of cyclesines and a settlines of the sixes and a settlines of 
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                                                                                                                                                                                                                                                                                               Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal vycosine methylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 7128 BP; 2031 A; 207 C; 1612 G; 3278 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 1531, 32pp + Sequence Listing, German
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ilarity 100.0%; Pred. No. 0.00045;
Conservative 0; Mismatches 0;
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                                                           Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABO67149 standard; DNA; 40324
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                                                           Olek A. Piepenbrock
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ABQ67149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Allen SM, Heppard BP, Sakai H, Weng Z, Helentjaris TG, Macool DJ;
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hes 0; Indels 0
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ive 0; Mismatches
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                                                                                                                       99WO-US29824.
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                                                                                                                       15-DEC-1999;
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22-JUN-2000.
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Best Local Si
Matches 34;
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                             The invention relates to a method of detecting human immunoditions, virile 2 models called [16] in a biological smaple by contexting Must multiple the property of the providing Must multiple the sequence, and detecting the amplitted Must providing hybridisation probe and detecting the amplitted Must be probe to the probe capts object, and detecting the Must be probe to the problem, and detecting the Must be provided to the problem of the problem of the must be provided and the problem of the must be provided to several the amplitude and types A. B. C and D of HIV. The method is useful for amplitude and types A. B. C and D of HIV. The method is useful for amplitude and types A. B. C and D of HIV. The method is useful for amplitude and types A. B. C and D of HIV. The method is useful for amplitude to the provided the must be applicated to the amplitude to the provided the must be described the amplitude to the amplitude to the provided the must be described the amplitude to the amplitude to the provided the amplitude to the amplitude to the provided the must be described to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting human immunodeficioncy virus-2 nucleic acids in a maple, a mapping human immunodeficioncy virus-2 nucleic acids and edetecting nucleic acid. Or hybridising nucleic acid with a probe and detecting nucleic acid.
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30-MAR-2001; 2001US-280058P-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeliciency virus type 2 detection probe #32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 40324 BP; 12279 A; 436 C; 8127
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HIV-2 detection probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 57; 58pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probe:target duplex
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2002-017408/02.

AAU69621

Barney

Portbury SD,

Puranam K,

Katz LC,

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(COGE-)

COGENT NEUROSCIENCE INC Thomas MB,

11-APR-2000; 2000US-0547596

Claim 2; Figure 6K; 256pp; English

Novel nucleic acids referred as protective sequences and their encoded products for diagnosing, treating diseases involving cell death, including neurological disorders e.g. stroke and for identifying

control relates to isolated protective sequence polypoptides (1) can delynomiate (11) it suefit for transferring protective sequence into a coll, which delays and/or prevent the coll free sequence into a coll, which delays and/or prevent the coll free control related to the coll collection of the co

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                       Human, protective sequence, cell death, carabral oodema, infection; maningitis degenerative disease; Alatham's disease, heart disease motor neuron disease, demyelinating disease; multiple scletonis; asthematicitionis, conditions, consistent mutritional, condition, peripheral nervous system desorter; bethematik;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1185 GTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 51 BP; 31 A; 8 C; 3 G; 9 T; 0 other;
09-APR-2001, 2001WO-US11655
                                                           18-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell death protective sequence CNI-00725, ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS63020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS63020 standard; cDNA; 116 BF
                                                                                                                W0200176532-A2
                                                                                                                                                                      Homo sapiens
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Similarity 100.0%;
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Pred. No. 0.0028
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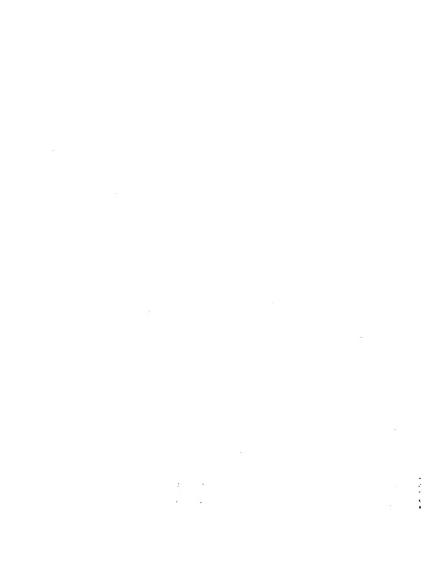
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(Googenita menalias) medianticos, haster (Grotton antitio), thyroid gland (Hashisocc's thyroidiantica stopph) hose atroo and the amenical parter (Hashisocc's thyroidiantica stopph) hose atroo a bose (settled parter (Hashisocc's thyroidiantica), hose atroo and are useful for compounds at Christian (Hashisocc's this dark and are useful for compounds at Christian (Hashisocc's this dark and are useful for compounds are churter to this for treating populational magnets on system caused by infection which induce coil death; (I) is useful to raise at a support this assay disapped to this assay disapped to this assay and appendix to the subject exceptions of the subject the subject exceptions of the subject to subject the subject to the subjec
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Search completed: December 17, 2002, 17:47:35 Job time : 310 secs



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sequence 11, Appl. Sequence 11, Appl. Sequence 15, Appl. Sequence 16, Appl. Sequence 18, Appl. Sequence 19, Appl. Sequence 19, Appl. Sequence 17, 
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tent No. 6294338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.8%; Score 34; DB 4; Length 57; Best Local Similarity 100.0%; Fred. Not. 1e-05; Indels Matches 34; Conservative 0; Mishatches 0; Indels Matches 34; Conservative 0; Mishatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/OS5258A

Reference 7, Application US/OS5258A

SEGUENCE CONTROLLER CONTRO
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-620-958A-7
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US-09-620-958A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-227-357-35
                      LENGTH: 57
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                                                                                                                                                                                                                                                                                                                                                                                                   December 17, 2002, 17:10:36; Search time 74 Seconds (withbot alignments) 5043:589 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a
coors greater than or equal to the score of the result bring printed,
and is derived by analysis of the total score distribution.
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                                                                               GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                            - nucleic search, using sw model
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Word Size
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-07-885-970A-13

CORRESPONDENCE ADDRESS:

ADDRESSEE: RATNER & PRESTIA STREET: P.O. BOX 980

CITY: VALLEY FORGE

STATE: PA COUNTRY: USA ZIP: 19482

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US-09-009-438-1
, Sequence 1, Application US/09009438
; Patent No. 5981223
                                                                                                                                                                                                                                                                  OY 1185 GTTTAAAAAAAAAAAAAAAAAAAAAAAAAA 1217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08379482A
Parent No. 5859334
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                  Ouery Match 2.7%; Score 33; DB 2; Length 1738;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 33; Conservative 0; Mismatches 0; Indels
GRIEDAL INPORMATION:
APPLICAMT: SATISE CAMESH M.
APPLICAMT: SATISE CAMESH M.
APPLICAMT: MEGGAM. DESK T.
TITLE OF INVENTION: MEGGAM. RECEPTOR
NUMBER OF EXQUENCES. 2
NUMBER OF EXQUENCES. 2
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TELEPAX: (516)742-4366
TELEX: 230 901 SAMS UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                   1667 GTTTABABABABABABABABABABABABABA 1699
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STATE: New York
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APPAICANT, MOLDON GIOCHTO,
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING
TITLE OF INVENTION: GLOCHITIANISFERASE ENZYMES AND USES THEREFOR
INDIRER OF SEQUENCES...?
                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1738 base pairs
TYPE; nucleic acid
STRANDEDNESS: single
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STREET: 400 Garden City Plaza
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APRICANT. IRREAD RESELVOA.
PRICANT. KROOR, AKCHAN.
TITLE OF INVENTION: NUCLEGOTION SEQUENCES COOLNG FOR THE
TITLE OF INVENTION SUCLESCIPLY SERVA-ARREMENCIC RECEPTOR AND THEIR APPLICATIONS
WORRES OF SEQUENCES: 9
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Patent No. 5656440
GENERAL INFORMATION:
       US-09-465-558-35
Patent No. 6436657
; Detent No. 643667
; GENERAL INPORMATION:
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TELEX: 248655 OPAT UR
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2000 base pairs
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Matches 33; Conserve
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STREET: 175
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2.7%; Score 33; DB 2; Length 1910;
Best Local Similarity 100 '08; Pred No. 1.9c-0. 2) Indels
Best factors 33; Conservative 0; Mismatches 0; Indels
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Person No. G
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Cy 1185 GTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1217
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                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
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TELEPHONE: 610-407-0701
TELEPHONE: 610-407-0701
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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7 MOLECULE TYPE: CDNA
US-09-009-438-1
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Matches 33; Conserva
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ORGANISM: Human
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US-09-207-493-1
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T-9162-008-80-S0
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                                                                                      Best Local
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Patent No. 6153740
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/499,314
FILING DATE: 7-JULY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Halls, Lide A.
REGISTRATION NUMBER: 38,347
REGISTRATION NUMBER: 38,347
TRIEGROMANICATION INFORMATION:
TELECHOME: 6,13/6/78-5070
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INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2790 base pairs
                              1185 GTTTARADAMAAAAAAAAAAAAAAAAAAAAA 1217
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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
2729 GTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 276:
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CITY: La Jolla
CTATE: CA
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FILING DATE: 13-FEB-
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMEDITES: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: J.D. Young
TITLE OF INVENTION: C
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                       BALUKE:
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LOCATION: 107..1321
LOCATION: 107..1321
OTHER INFORMATION: /function= "BOVINE BETA-3 RECEPTOR"
OTHER INFORMATION: /product= "ADRENERGIC, BETA RECEPTOR"
                                                                       hes 33; Conserv
                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                     LOCATION:
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4225 Executive Square, Suite 1400
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                                                                   2.7%; Score 33; DB 3; L
(larity 100.0%; pred. No. 1.9e-05;
Conservative 0; Mismatches 0;
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N: cDNA ENCODING NUCLEOSIDE TRANSPORTER
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100.0%, Pred. No. 1.9e-05
active 0; Mismatches 0
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US-09-020-956-110
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, Patent No. 6316698
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Patent No. 6261562
GENERAL INFORMATION:
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APPLICANT MINER, ARCHON, J.
APPLICANT MINER, ARCHON, J.
APPLICANT MINER, ARCHON, J.
APPLICANT MINER, M. APPLICANT, J.
APPLICANT APPLICATION AND ARCHARGA (MARCHARGA MARCHARGA MARCH
                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 3410 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 09-FEB-1398
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: NAME, DAVId 31.392
REGISTRATION HAMBER: 31.392
REGISTRATION HAMBER: 32.101
TREFERENCE/INFORMETION: TREMENDATION: TREMENDATION: TREMENDATION: TREMENDATION: 10.2001 02.21.900
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ORGANISM: Glycine max
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                                                                                                                      ORIGINAL SOURCE
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MEDITAM YTES - 190py disk
COMPUTES: 18M PC compatible
COMPUTES: 18M PC compatible
COMPUTES: 18M PC compatible
OPERANTING SYSTEM, PC-105/MS-10S
SOPTHARE: PRESENT NCT-18M PS-1.0, Version #1.30
APPLICATION MOMERS: US/99/020,956
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APPLICANT: Dillin, Davin
                                                                                                                                                                                                                                            TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
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                                                    Homo sapiens
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100.0%; Pred. No. 1.8e-05;
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ADDITION: COMPOSITION ADDITION

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No. 1.8e-05; Matches 33; Conservative 0; Mismatches 0; Indels
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, Sequence 110, Application US/09352616A
                                                                                                                                                                                                                                                                              Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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, ORGANISM: Homo sapien
US-09-605-785-110
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Parent No. 25
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STREET: 6300 Columbia Center, 701 Fifth Avenue
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Patent No. 6321716
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                                     Sequence 217, App Sequence 217, App Sequence 217, App Sequence 110, App Sequence 111, App Sequence 111
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99.6%; Pred. No. 1.4e-55;
ative 0; Mismatches 1; Indels
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OTHER TRICRMANTON: Incyte ID No. US20020013958A1 700159305H1
UG-09-223-876-1860
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      Best Local Similation
Matches 225, Conservative
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9 (1971) 4 (Prodes at 2) (Julipay 1898) PUBCODS seqt.

11 (1971) 4 (Prodes at 2) (Julipay 1898) PUBCODS seqt.

12 (1972) 4 (Prodes at 2) (Julipay 1898) PUBCODS seqt.

13 (1972) 5 (Prodes at 2) (Julipay 1898) PUBCODS seqt.

14 (1972) 5 (Prodes at 2) (Pubpay 1898) PUBCODS seqt.

15 (1972) 6 (Prodes at 2) (Pubpay 1898) PUBCODS seqt.

16 (1972) 6 (Prodes at 2) (Pubpay 1898) PUBCODS seqt.

17 (1972) 6 (Prodes at 2) (Pubpay 1898) PUBCODS seqt.

18 (1972) 7 (Prodes at 2) (Pubpay 1898) PUBCODS seqt.

19 (1972) 7 (Prodes at 2) (Pubpay 1898) PUBCODS seqt.

19 (1972) 7 (Pubpay 1898) PUBCODS seqt.

19 (1972) 7 (Prodes at 2) (Pubpay 1898) PUBCODS seqt.

19 (1972) 7 (Prodes at 2) (Pubpay 1898) PUBCODS seqt.

19 (1972) 7 (Pubpay 1898) P
                                     GenCore version 5.1.3
Copyright (c) 1993 - 2002 Computen Ltd.
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                                                                                                                                                            nucleic search, using sw model
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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; ORGANISM: Homo sapiens
US-09-925-297-257
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                                                                                                                                                                     Query Match
Best Local Similarity
Matches 34, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.1
SEO ID NO 31
LENGTH: 57
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Patent No. US20020055095A1
GENERAL INFORMATION:
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GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT, Rosen e. al.
TITLE OF INFERTION Nucleic Acids, Proteins and Antibodies
File Reference: PAIGS
FILE REFERENCE: PAIGS
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APPLICANT BEREVALOS Seem T.
APPLICANT PRAW MANDALS
APPLICANT PRAW MANDALS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEC ID NOS: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/229,790
PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: Capture OTHER INFORMATION: oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1182 TTCGTTTAAAAAAAAAAAAAAAAAAA 1217
                                                                                                       1184 CGTTTAAAAAAAAAAAAAAAAAAAAAAAAAAA 1217
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                                         23 CGTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 56
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hes 36; Conserv
                                                                                                                                                                     2.8%; SCORE 34; DB 10;
ilarity 100.0%; Pred. No. 0.0008;
Conservative 0; Mismatches 0
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100.0%; Pred. No. 7.1e-05;
ative 0; Mismatches 0; Indels
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; Sequence 9612, Application US/09867701
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US-10-001-407-32
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                                                                                                       Patent No. US20020132237A1
GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 32
LENGTH: 51
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Best Local Similarity 100.0%;
Matches 34; Conservative (
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Patent No. US20020177127A1
GENERAL INFORMATION:
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Patent No. US20020106668A1
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CURBENT FILMS ANTE: 2001-10-22
PRIOR APPLICATION NUMBER: 60/242,520
PRIOR APPLICATION NUMBER: 60/280,058
APPLICANT, HAT-locker, Susan L.
TITLE OF INVENTION: OANDOSTITUS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Burrell, Terrie
TITLE OF INVENTION: Compositions and Methods for Detecting
TITLE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)
FILE REFERENCE: GP117-03.UT
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ORGANISM: Artificial Sequence
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Length 51;

Indels

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Gaps

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; OTHER INFORMATION: Sequence of the (-)4258 A30 capture probe US-09-943-286-7
                    2.8%; Score 34; DB 10; Length 57
     Indels
0;
     Gaps
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measure, 18-23-1890; catton 18/09860382

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          APPLICATE, BERNAR, PRESENCE SEQUENCES OF ARBIDIODES STILLS OF INVESTIONS EXCESSED AND ASSESSED AS ASSESSED.
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ORGANISM: Bos taurus
OTHEN INFORMATION: Clone ID: 23-LIB34-026-Q1-E1-F3
US-09-560-353-8390
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Patest No. US/020062014A1
GENERAL INFORMATION:
APPLICANT: GOTLASH, JOHN
APPLICANT: AN, YONG-Qiang
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Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
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ORGANISM: Arabidopsis thaliana
US-09-770-791-608
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Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
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Rameaka, Joshua G.
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LENGTH: 356
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2.7%; Score 33; DB 10; Length 178;
Bet Local Similarity 100.0%; Pred. No. 0.0015.
Matches 33; Conservative 0; Mismatches 0; Indels
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FILE REPREMENCE 121021-49
CURRENT AFPLICATION NAMER: US/09/867,701
CURRENT FILING NATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912 OF WINDOWS VERSION 4.0
SUCTINATE: FREEED FOR MINDOWS VERSION 4.0
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Patent No. US20020132237A1
GENERAL INFORMATION:
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Matthew, Abraham V.
Ledford, Brooke L.
Nossener, Jeffrey P.
Hass, William David
Garcia, Carlos A.
Slader, Ted
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Allen, Keith
Hoffman, Neil
                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapien
US-09-867-701-9612
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US-09-867-701-10381/c
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                                                                                                                                                                                                                                                                                                              LENGTH: 178
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RESULT 12
US-09-924-035A-B99/c
US-09-924-035A-B99/carion US/09924035A
Sequence 899, Application US/09924035A
Patent No. US20020142319A1
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Sequence 243, Application US/09867701
Patent No. US20020132277A1
GENERAL INFORMATION:
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US-09-770-791-242
GENERAL INFORMATION:
APPLICANT: GTICH, Jrn
TITLE OF INVENTION: EXpressed Sequences of Arabidopsis
TITLE OF INVENTION: Chaliana
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LENGTH: 376
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NAME/KEY: misc feature
LOCATION: (1)...(413)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33; Conservative
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Allen, Keith
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Slader, Ted
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100.0%; Pred. No. 0.0013;
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100.0%; Pred. No. 0.0013;
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                                         US-09-770-149-485
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; ORGANISM: Arabidopsis thaliana
US-09-924-035A-899
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SEQ ID NO 886
LENGTH: 609
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CURRENT FILING DATE: AD00-08-11
PRIOR PRILICATION NUMBER: U8 60/148,784
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 9,00
SOFTMARE: PRESEQ FOR MINDOWN Version 3.0
SOFTMARE: OBSEQ TO MINDOWN Version 3.0
SEQ ID TUNO 899
SEQ ID TUNO 899
        Sequence 485, Application US/09770149
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Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 33; Conservative 0; Mismatches 0; Indels
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Patent No. US20020059663A1
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                                                                                                                                                                                                     61 GTTTAVAAVAAAAAAAAAAAAAAAAAAAAAAA 29
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Davis, Keith R.
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Ledford, Brooke L.
Noessner, Jeffrey P.
Naes, William David
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Slader, Ted
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Rameaka, Joshua G.
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Hamilton, Carol M.
Price, Jennifer L.
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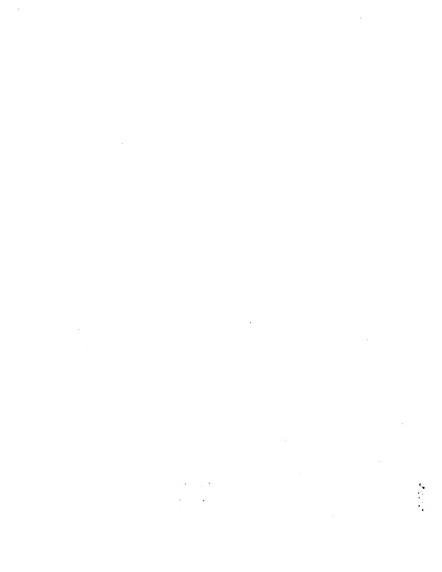
0; Mismatches

Matches 33; Conservative

Patent No. US20020059663A1

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Oy 1185 GTTTARADARADARADARADARADARADA 1217
                                                                             836 GTTTRARARARARARARARARARARARA 868
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Job time : 87 secs
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| NAME/KEY: misc_feature
| LOCATION: (1) - . (659)
| OTHER INPOMATION: n = A,T,C or G
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ORGANISM: Arabidopsis thaliana
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ORGANISM: Homo sapiens
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.	- nucleic search, using sw model	December 17, 2002, 15:59:41 ; Search time : (Without alignmy 8198.797 Million	US-09-720-384A-3 1217 1217	OLIGO NUC Garon 60.0 . Garoext 60.0	16154066 segs, B097743376 residues	0	Total number of hits satisfying chosen parameters: 32	seq length: 0 seq length: 2000000000	Post-processing: Listing first 45 summaries	EST:* 1: em estba:*	2: em_esthum:* 3: em_esthum:* 4: em_esthum:*	1: em_eatur. 5: em_eatur. 6: em_eatur.*	7: em_estro:* 8: em_htc:*	9: gb estl:* 10: gb est2:* 11: ab htc:*	12: gp_est3.* 13: gp_est4.* 14: gp_est4.*	19: 90 est5: 15: em_estfun:* 16: cm_estcm:*	18: em_ges_hum:* 19: em_ges_inv:*	20: em_gss_pin:* 21: em_gss_vr:* 22: em_gss_fun:*	23: em_gas_mam:* 24: em_gas_mus:* 25: em_gas_other:*	26: em_gss_pro:* 27: em_gss_rod:*	is the rater than	SUMMARIES	Guery Match Length DB ID	11.5 615 11 AY108005 11.3 627 10 AM052991 9.7 591 12 BG871962 8.9 272 10 AM28601 8.3 736 T BH35239 6.0 675 10 BR347376
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614077E08 x3 614 - root cDNA library from Walbot Lab Zea mays cDNA,
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Tel: 650 723 2227
Fax: 650 725 8221
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Department of Biological Sciences
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Spermatophyta, Magnoliophyta, Liliopuida; Poales; Poaceas; PACC
clade, Pantocidea; Andropogoneas; Zea.
1, (bases 1 to 627)
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Plate: 614077 row: E col
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BACKWARD: T3 (ATT AAC CCT CAC TAA
Seg primer: primer T3 (ATT AAC CCT
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Tel: 515-294-0975
Fax: 515-294-2299
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MEST44-F08.T3 ISUM4-TN Zea mays cDNA clone MEST44-F08.3', mRNA
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                                decINA molecule; pr779PGC, Step_1: ExoRi; Step_2: Not; decINA molecule were generated as Collows Framerum (ACMA molecule were desired with Names H and used you have remarked as Collows Framerum (ACMA molecule were discretionally decided with those and size selected. The resulting molecules were discretionally collows from the collows were discretionally collows.
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Zee mayor Viridiahanten Ersprophyte, Debryphyte, Fordensphyte, Spransen, Stransen, Str
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BH839239 736 bp DNA linear GSS 28-NAY-2002
LMCR150009G06f Zea mays L. Zea mays genomic clone LMCR150009G06f,
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212 CGAACCACCATTAATGGTGAGATAGTAATTAAGATGAAAGATGGGGAATGCCCTTCACC 153
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Query Match

10.04, Pred. No. 1.3e-44,

Matches 101, Conservative 0, Mismatches 0, Indels 0
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High quality sequence stop: 713.
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Poulse (organism Scophum Exclor (OI)*  (d) xee* twonising (OI)*  (close lin* bark Grown 1 (OI)*  (arcse Organis Samp And Old dark grown seedlings; ) Vector:  (arcse Organis Samp And Old dark grown seedlings; ) Vector:  made from poly A Bob in the closing vector landes AP II.	ODMSMAL ORDERING ACCOUNTRACE AND COMMENT OF THE COMMENT AND COMMENT LABORAGOUT FOR GROWING AND BOINTCORNALCH THE University of Georgia, Department of Flant Biology Plant Sesionce Building, Rm. 2502, Athens, GA 30602-7277, USA Pair 706 524 2650 Pair 706 524 2650 Pair 706 534 2650
L CELEBOT	
seq primer: polyPMix High quality sequence start: 64 High quality sequence stop: 697 nigh quality	The Author Control of the Control of
Emall: mmpratt@ags.edu Sequences have been trimmed to exclude PolyA, vector and regions Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence	3
Plant Sciences Building, Rm. 2002, Athems, GA 36602-7271, USA 761: 706 542 1860 Fax: 706 543 0210	ACCESSION BEJ55111. GI:9296311  KEYMORDS EST. 31. GI:9296311
JOURNAL Unpublished (2000)  COMMENT Contact: Coctoonie-Pratt MM Laboratory for Genomics and Bioinformatics  The District of Contact and Bioinformatics  Th	8
An EST database from Sorghum: dark-grown seedlings	RESULT 7
spermatophyta, Magnollophyta, Lillopaida, Poales; Poaceae, PACC clade; Panicoidese, Andropogonese; Sorghum.  EFFRENCE 1 (bases 1 to 699) Andropogonese; Sorghum.  ATTHINGS Cordonies-Port M. M. Ginola A. Marsala C. Sudman M. and Pratt	OY 693 CANACCTUTTOC 705 Db 228 CANACCTUTTOC 240
SOURCE SOZIMUM BIOLOGICA SOZIM	OY 63 GAGATTAAGCTTAAGCCACHAGCCGTGCHGAAAAATRACCAHAGAGTGCHAATEG 892 Db 168 GAGATTAAGCTTTAAGGCAGAGAGCCGTGCHGAAAATRATCGAAGAGTTGGTGAAGTGG 227
N BE361874.1 GI:9303431	Matchee 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
699 bp mRNA linear EST 20-U 5.gl_A002 Dark Grown 1 (DG1) Sorghum bicolor cDNA,	y Match
T 8	Clones to be seguenced were prepared by mass excision."  BASE COUNT 207 a 121 c 161 g 186 t  ORIGIN
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Qy 63 GAGATTEAAGCCAGAAGACCCTCCAGAAAATREACGAGAGGTCTCGAGAGGC 692  Db 161 GAGATTEAAGCCAGAAGACCCTCCAGAAAATREACGAAGAGTTGGTCAAGTCG 220	org Loca
Derry March (6.04, Score 73; DB 10; Length 691; Best Local Similarity 100.04; Ped. No. 3 66-08; Marches 73; Conservative 0; Mismarches 0; Indels 0; Gaps 0;	Se of thems: PolyPHM; High quality sequence start; 30 High quality sequence stop; 638 PolyNaNo.
made from poly-A RaW in the cloning vector landed RAF II.  Clones to be adequanced were prepared by mass excision.*  124 c 167 g 188 t	Fax: 706 583 0210  Fax: 706 583 0210  Small: impractegal edu  Small: impracteg
/organisms-Socyphus bicolor: /organisms-Socyphus bicolor: /organisms-behave down   (oct)* /organisms-behave down   foct)* /organisms-behaved dark-grown seedlings:/voctor: /organisms-behaved dark-grown seedlings:/voctor: /organisms-behaved dark-grown seedlings:/voctor: /organisms-behaved dark-grown seedlings:/voctors-behaved-general-	
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Seq primer: PolyfMix High quality sequence start: 23 High quality sequence stop: 682 non; Michael Sequence Stop: 682	clade, Panicoidese, Andropogonese; Sorghum. REFERENCE 1. (bases L. t. 6.75) AUTHORS Cordonnier-Pratt, MW., Gingle, A., Mareala, C., Sudman, M. and Pratt
Email: emprettaugs.edu George de de la company it the control of the company of the control of the company is the control of the company of the control of t	SOURCE socghum : COLOr COMMUNICATION COMMUNI

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see Building, Rm. 2502, Athens, GA 30602-7271, USA
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att.M.-M., Gingle,A., Marsela,C., Sudman,M. and Pratt
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100.0%; Pred. No. 3.6e-08;
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e="Organ: 5-day-old dark-grown seedlings; Vector:
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da Zap; Site_l: XhO; Site_2: Eco8; The library vs
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Plant Biology
University of Illinois
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Stanford University
855 California Ave, Palo Alto, CA
                                                                                                                                                                                                                                                                                                                                                       1201 W Gregory Dr. Urbana, IL 61801,
Tel: 2172655473
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Plate: 614055 row: F colu
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                                                                                                                                                                                                                                                                                                                           Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hordeum vulgare.
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/clone_lb="HC"
/tissue_type="Root"
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/Clone_lb=*G14 - root cDNA library from Walbot Lab*
/flsmel_type=*root*
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//ab/_bost=*/KOLS**
//ab/_bost=*/KOLS**
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ECGRI, Site_2: XhOI; 3-4 days old root tissue from Walbot
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/strain="cv tokak"
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/cultivar="W23"
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Bmail: mmpratt@uga.edu
Bmail: mmpratt@uga.edu
Goognunces have ben trimmed to exclude PolyA, vector and regions
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales; Poaceae; PACC clade, Panicoideae, Andropogoneae; Sorghum.

I (bases I to 169)
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Spermatophyta; Megnoliophyta "Liliopaida, Poales; Poaceas; PACC
Cade Panicolophyas; Andropogoneas; Sorghum.
1. (basee 1 to 162)
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An EST database from Sorghum: dark-grown seedlings
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